CLAIMS

1. An isolated protein comprising at least a subsequence of the amino acid sequence of LTA_4 hydrolase, which exhibits a three-dimensional form essentially as disclosed in Table 9 by the parameters defining atom 1 to atom 4876, said subsequence being capable of participating in the control of the an enzymatic pathway, such as the leukotriene cascade, or a functionally equivalent part, derivative or conformational analogue thereof.

2. A protein according to claim 1, which comprises an enzymatically active site defined in the following table:

	Left wall	Right wall
1		Lys608, Asp606, Lys605, Lys354, Thr355
2	Phe356, Phe362	Gln544, Asp573, Lys572, Arg568
3	Val376	Lys565, Arg540, Leu507
4	Ser380, Ser352, Glu348	Pro569
5	Tyr378, Glu348	Arg563, Glu533, Phe536, Arg537, Tyr267
6	Tyr383, Phe314, Glu318, Glu384, Arg326	
7	Gly268, Gly269, Met270	His295, Asn341, Phe340
8	Ser288, His497	Glu325, Asn291

3. A protein according to claim 2, which is an enzyme having a metallohydrolase activity capable of participating in the regulation of enzyme activities in biochemical pathways, wherein said enzymes have structures similar to the ones defined in claim 2.

4. A protein according to claim 1, which comprises an enzymatically active site defined by the following amino acids: Gln136; Ala137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Glu318; Tyr378; Tyr383; Arg563; Lys565.

5. A protein according to claim 1, which comprises an enzymatically active site defined by the following amino acids: Gln136; Ala137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Trp315; Glu318; Val322;

Phe362; Val367; Leu369; Pro374; Asp375; Ile372; Ala377; Pro382; Tyr378; Tyr383; Arg563; Lys565.

6. A compound which is substantially complementary to a protein according to any one of claims 1-5.

7. A compound according to claim 6, which is substantially complementary to an enzymatically active site of said protein and which is capable of specifically inhibiting said enzymatic activity.

8. A compound according to claim 7, which is an inhibitor of a metallohydrolase enzyme.

9. An isolated complex, which is comprised of a protein according to claim 1-5 and a complementary compound according to any one of claims 6-8, wherein the three-dimensional structure of LTA_4 hydrolase is essentially as disclosed in Table 9 by the parameters defining atom 1- atom 4876, or a functionally equivalent part, derivative or conformational analogue of such a complex.

10. A complex according to claim 9, wherein the protein complexed with LTA_4 hydrolase is selected from the group which consists of bestatin, thiolamine or hydroxamic acid, or a functionally equivalent part, derivative or conformational analogue of such a complex.

11. Use of the parameters of a protein according to any one of claims 1-5, a compound according to any one of claims 6-8 or a complex according to claim 9 or 10 in drug design, such as in molecular modeling, direct structure-based design and/or combinatorial chemistry.

12. Use according to claim 11, wherein said parameters are selected from the parameters disclosed in Table 9 defining atom 1- atom 4876.

13. Use according to claim 11 or 12, wherein said drug is for the treatment and/or prevention of disorders involving acute and chronic inflammatory and/or allergic symtoms, said disorder being selected from the group consisting of arthritis, inflammatory bowel disease (IBD), psoriasis, chronic obstructive pulmonary disease (COPD), and acquired immune deficiency syndrome (AIDS).

14. Use according to claim 11 or 12, wherein said drug is for the treatment and/or prevention of proliferative disorders, such as neoplasias and/or cancer.

15. Use according to claim 11 or 12, wherein said drug is for the treatment and/or prevention of disorders caused by the lethal factor of *Bacillus anthracis*, e.g. anthrax.

16. A method for screening LTA_4 hydrolase analogues that mimic at least a part of the three dimensional structure of the LTA_4 hydrolase molecule as defined by the parameters shown in Table 9 for atom 1 to atom 4876, which comprises the steps of

(a) producing a multiplicity of analogue structures of LTA_4 hydrolase and

(b) selecting an analogue structure, wherein the three-dimensional configuration and spatial arrangement of one or more enzymatically active sites and/or binding sites of said LTA_4 hydrolase remain substantially preserved.

17. A method according to claim 16, wherein an analogue exhibiting an enzymatic activity, such as an epoxide hydrolase and/or aminopeptidase activity, is selected.

18. A method according to claim 16 or 17, wherein an enzymatic inhibitor complementary to the amino acids defined in any one of claims 3, 4 or 5 is screened for.

19. An analogue obtainable by the method according to any one of claims 16-18.

20. An analogue according to claim 19, which exhibits an increased catalytic activity when compared to the naturally occurring form of LTA_4 hydrolase, such as defined in Table 9 by parameters of atom 1 to atom 4876.

21. A method for screening LTA_4 hydrolase binding compounds complementary to a region of LTA_4 hydrolase, preferably an enzymatically active site thereof, which comprises the steps of

(a) producing a multiplicity of possible complementary structures and

(b) selecting a structure, wherein the three-dimensional configuration and spatial arrangement of regions involved in binding to LTA_4 hydrolase remain substantially preserved, which selection is based on the three-dimensional structure of LTA_4 hydrolase, and/or LTA_4 hydrolase complexed to an inhibitor thereof, in a form adopted thereof in nature, such as defined in Table 9.

22. A method according to claim 21, wherein a general metallohydrolase inhibitor is selected, which is capable of inhibiting an enzyme belonging to the M1 family.

23. A method according to claim 21, wherein an inhibitor of the epoxide hydrolase activity and/or aminopeptidase activity of LTA_4 hydrolase or of LTC_4 synthases is selected.

24. A method according to claim 21, wherein a compound capable of antagonizing LTB_4 receptor binding of a cell is selected.

Sub A6 25. A compound obtainable by the method according to any one of claims 21-24.

26. A method of engineering a protein, which method comprises the steps of

-identification of a suitable set of mutations based on the structure of LTA_4 hydrolase;

-generation of a library of genes which contains the suitable sequence variations;

-selection of clones encoding the LTA_4 hydrolase analogues with a desired activity function;

wherein said desired activity is the capability of efficiently producing an organic compound of interest.

27. A method according to claim 26, wherein the specified property is the suicidal mode of action of LTA_4 hydrolase.

Sub A7 28. A process for the purification of a protein according to any one of claims 1-3 or obtained according to claim 26 or 27, which purification includes hydroxyapatite-based chromatography and a subsequent anion exchange chromatography.

29. A process for the crystallisation of an LTA_4 hydrolase, an analogue or a derivative thereof, wherein said crystallisation is performed with the addition of a ytterbium salt as an additive, such as an ytterbium chloride.

Sub A8 30. A protein obtained by the method according to any one of claims 27-29.

31. A protein according to claim 30, which is present in an essentially pure form.

32. An isolated nucleic acid encoding a protein according to claim 30 or 31.

33. A nucleic acid capable of specifically hybridising to a the nucleic acid according to claim 32.

34. Use of a protein, which is a genetically modified LTA_4 hydrolase, according to claim 30 or 31 in the preparation of LTB_4 or other metabolites in the leukotriene cascade.

35. A protein according to any one of claims 6-8, 25, 30 or 31 for use as a medicament.

36. Use of a protein according to any one of claims 6-8, 25, 30 or 31 in the manufacture of a medicament for the treatment and/or prevention of acute and chronic inflammatory and/or allergic disorders, said disorder being selected from the group consisting of arthritis, inflammatory bowel disease (IBD), psoriasis and chronic obstructive pulmonary disease (COPD); neoplasias and/or cancer; or disorders caused by the lethal factor of *Bacillus anthracis,* e.g. anthrax.

37. Use of a protein according to any one of claims 6-8, 25, 30 or 31, in the manufacture of a medicament for the treatment and/or prevention of an anti-inflammatory and/or anti-allergenic disorder, such as bronchial asthma, allergic rhinitis, conjunctivitis etc.

38. Use of a protein according to any one of claims 6-8, 25, 30 or 31 in the manufacture of a medicament for the treatment and/or prevention of infection caused be human immunodeficiency virus (HIV).